

## FIGURE 1

GGACTAATCTGTGGGAGCAGTTTATTCCAGTATCACCCAGGGTGCAGCCACACCAGGACTGT  
GTTGAAGGGTGTTTTTTTTCTTTTAAATGTAATACCTCCTCATCTTTTCTTCTTACACAGTG  
TCTGAGAACATTTACATTATAGATAAGTAGTACATGGTGGATAACTTCTACTTTTAGGAGGA  
CTACTCTCTTCTGACAGTCCTAGACTGGTCTTCTACACTAAGACACCATGAAGGAGTATGTG  
CTCCTATTATTCTGGCTTTGTGCTCTGCCAAACCCTTCTTTAGCCCTTCACACATCGCACT  
GAAGAATATGATGCTGAAGGATATGGAAGACACAGATGATGATGATGATGATGATGATGATG  
ATGATGATGATGAGGACAACCTCTCTTTTTTCCAACAAGAGAGCCAAGAAGCCATTTTTTTTCCA  
TTTGATCTGTTTCCAATGTGTCCATTTGGATGTCAGTGCTATTACGAGTTGTACATTGCTC  
AGATTTAGGTTTGACCTCAGTCCCAACCAACATTCCATTTGATACTCGAATGCTTGATCTTC  
AAAACAATAAAATTAAGGAAATCAAAGAAAATGATTTTAAAGGACTCACTTCACTTTATGGT  
CTGATCCTGAACAACAACAAGCTAACGAAGATTACCCAAAAGCCTTCTAACCACAAAGAA  
GTTGCGAAGGCTGTATCTGTCCCAATCAACTAAGTGAAATACCACTTAATCTTCCCAAAT  
CATTAGCAGAACTCAGAATTCAATGAAAATAAAGTTAAGAAAATACAAAAGGACACATTCAAA  
GGAATGAATGCTTTACACGTTTTTGGAATGAGTGCAAACCCTCTTGATAATAATGGGATAGA  
GCCAGGGGCATTTGAAGGGGTGACGGTGTTCATATCAGAATTGCAGAAGCAAACTGACCT  
CAGTTCCTAAAGGCTTACCACCAACTTTATTGGAGCTTCACTTAGATTATAATAAAATTTCA  
ACAGTGGAACCTTGAGGATTTTAAACGATACAAAGAACTACAAAGGCTGGGCCTAGGAAACAA  
CAAAATCACAGATATCGAAAATGGGAGTCTTGCTAACATACCACGTGTGAGAGAAATACATT  
TGGAACAATAAACTAAAAAAATCCCTTCAGGATTACCAGAGTTGAAATACCTCCAGATA  
ATCTTCCTTCATTCTAATTCAATTGCAAGAGTGGGAGTAAATGACTTCTGTCCAACAGTGCC  
AAAGATGAAGAAATCTTTATACAGTGCAATAAGTTTATTCAACAACCCGGTGAAATACTGGG  
AAATGCAACCTGCAACATTTTCGTTGTGTTTTGAGCAGAATGAGTGTTTCAGCTTGGGAACTTT  
GGAATGTAATAATTAGTAATTGGTAATGTCCATTTAATATAAGATTCAAAAATCCCTACATT  
TGGAATACTTGAACCTCTATTAATAATGGTAGTATTATATATACAAGCAAATATCTATTCTCA  
AGTGGTAAGTCCACTGACTTATTTTATGACAAGAAATTTCAACGGAATTTTGCCAAACTATT  
GATACATAAGGGGTTGAGAGAAACAAGCATCTATTGCAGTTTCCTTTTTTGCGTACAAATGAT  
CTTACATAAATCTCATGCTTGACCATTCCCTTCTTCATAACAAAAAAGTAAGATATTCGGTA  
TTTAACACTTTGTTATCAAGCACATTTTAAAAAGAACTGTACTGTAAATGGAATGCTTGACT  
TAGCAAAATTTGTGCTCTTTCATTTGCTGTTAGAAAAACAGAATTAACAAAGACAGTAATGT  
GAAGAGTGCATTACACTATTCTTATTCTTTAGTAACTTGGGTAGTACTGTAATATTTTTAAT  
CATCTTAAAGTATGATTTGATATAATCTTATTGAAATTACCTTATCATGTCTTAGAGCCCGT  
CTTTATGTTTAAAACTAATTTCTTAAAAATAAAGCCTTCAGTAAATGTTTATTACCAACTTGA  
TAAATGCTACTCATAAGAGCTGGTTTGGGGCTATAGCATATGCTTTTTTTTTTTTTAATTATT  
ACCTGATTTAAAAATCTCTGTAAAAACGTGTAGTGTTTCATAAAATCTGTAACTCGCATTTT  
AATGATCCGCTATTATAAGCTTTTAAATAGCATGAAAATTGTTAGGCTATATAACATTGCCAC  
TTCAACTCTAAGGAATATTTTTGAGATATCCCTTTGGAAGACCTTGCTTGGAAGAGCCTGGA  
CACTAACAATTCTACACCAAATTTGTCTCTTCAAATACGTATGGACTGGATAACTCTGAGAAA  
CACATCTAGTATAACTGAATAAGCAGAGCATCAAATTAAACAGACAGAAACCGAAAGCTCTA  
TATAAATGCTCAGAGTTCTTTATGTATTTCTTATTGGCATTCAACATATGTAAAATCAGAAA  
ACAGGGAAATTTTCATTAAAAATATTGGTTTGAAAT

446460 "030" 446460

## **FIGURE 2**

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA34392

<subunit 1 of 1, 379 aa, 1 stop

<MW: 43302, pI: 7.30, NX(S/T): 1

MKEYVLLLFLALCSAKPFFSPSHIALKNMMLKDMEDTDDDDDDDDDDDDDDDEDNSLFPTREPR  
SHFFPFDLFPMPFCGQCYSRVVHCSDLGLTSVPTNIPFDTRMLDLQNNKIKEIKENDFKGL  
TSLYGLILNNNKLTKIHPKAFLTTKKLRRLYLSHNQLSEIPLNLPKSLAELRIHENKVKKIQ  
KDTFKGMNALHVLEMSANPLDNNGIEPGAFEGVTVFHIRIAEAKLTSVPKGLPPTLLELHLD  
YNKISTVELEDFKRYKELQRLGLGNNKITDIENGLANIPRVREIHLENNKLKKIPSGLP  
KYLQIIFLHSNSIARVGVNDFCPTVPKMKKSLYSAISLFNNPVKYWEMQPATFRCVLSRMSV  
QLGNFGM

### **Signal sequence.**

amino acids 1-15

### **N-glycosylation site.**

amino acids 281-285

### **N-myristoylation sites.**

amino acids 129-135, 210-216, 214-220, 237-243, 270-276, 282-288

### **Leucine zipper pattern.**

amino acids 154-176

0944944 083101

0944944 033031

CGGACGCGTGGGCGGACGCGTGGGGCCGCSGCACACGCCCGGCCCGCCCTCCGCCCTCCGCACTCGCGCTCC  
CTCCCTCCGCCCCGCTCCCGCGCCCTCCTCCCTCCCTCCTCCCCAGCTGTCCCGTTTCGCGTCAATGCCGAGCCTCCC  
GGCCCCCGCGGCCCGCTGCTGCTCCTCGGGCTGCTGCTGCTCGGCTCCCGGCCGGCCCGCGGCGCCGCCAGA  
GCCCCCGTGTGCCCATCCGTTCTGAGAAGGAGCCGCTGCCCCGTTTCGGGGAGCGGCAGGCTGCACCTTCGGCGG  
GAAGGTCTATGCCCTTGGACGAGACGTGGCACCCGGACCTAGGGCAGCCATTTCGGGGTGATGCGCTGCGTGCTGTG  
CGCCTGCGAGGCGCCTCAGTGGGGTCGCCGTACCAGGGGCCCTGGCAGGGTACAGTGCAGAAGACATCAAACCAGA  
GTGCCCCAACCCCGGCCTGTGGGCAGCCGCGCCAGCTGCCGGGACACTGCTGCCAGACCTGCCCCAGGAGCGCAG  
CAGTTCGGAGCGGCAGCCGAGCGGCCTGTCTTCGAGTATCCGCGGGACCCGGAGCATCGCAGTTATAGCGACCG  
CGGGGAGCCAGGCGCTGAGGAGCGGGCCCCGTGGTGACGGCCACACGGACTTCGTGGCGCTGCTGACAGGGCCGAG  
GTGCGAGGCGGTGGCACGAGCCCCGAGTCTCGCTGCTGCGCTCTAGCCTCCGCTTCTCTATCTCCTACAGGCGGCT  
GGACCGCCCTACCAGGATCCGCTTCTCAGACTCCAATGGCAGTGTCTGTTTGAGCACCTTCAGCCCCCACCCA  
AGATGGCCTGGTCTGTGGGGTGTGGCGGGCAGTGCCCTCGGTTGTCTCTGCGGCTCCTTAGGGCAGAACAGCTGCA  
TGTGGCACTTGTGACACTCACTCACCTTCAGGGGAGGTCTGGGGGCCCTCTCATCCGGCACCGGGCCCTGGCTGC  
AGAGACCTTCAGTGCCATCCTGACTCTAGAAGGCCCCCCACAGAGGGCGTAGGGGGCATCACCTGCTCACTCT  
CAGTGACACAGAGGACTCCTTGCATTTTTTGCTGCTCTTCCGAGGGCTGCTGGAACCCAGGAGTGGGGGACTAAC  
CCAGGTTCCCTTGAGGCTCCAGATTCTACACCAGGGGCAGCTACTGCGAGAACTTCAGGCCAATGTCTCAGCCCCA  
GGAACCAGGCTTTGCTGAGGTGCTGCCCCAACCTGACAGTCCAGGAGATGGACTGGCTGGTGCTGGGGGAGCTGCA  
GATGGCCCTGGAGTGGGACGGCAGGCCAGGGCTGCGCATCAGTGGACACATTGCTGCCAGGAAGAGAGCTGCGACGT  
CCTGCGAAAGTGTCTTTGTGGGGCTGATGCGCTGATCCCTGATCCAGTCCAGACGGGTGCTGCCGGCTCAGCCAGCTCAC  
GCTGCTAGGAAATGGCTCCCTGATCTATCAGGTGCAAGTGGTAGGGACAAGCAGTGAGGTGGTGCCATGACACT  
GGAGACCAAGCCTCAGCGGAGGGATCAGCGCACTGTCTGTGCCACATGGCTGGACTCCAGCCAGGAGGACACAC  
GGCCGTGGGTATCTGCCCTGGGCTGGGTGCCCGAGGGGCTCATATGCTGCTGCAGAATGAGCTCTTCTCTGAACGT  
GGGCACCAAGGACTTCCAGACGGAGAGCTTCGGGGGACAGTGGCTGCCCTGCCCTACTGTGGGCATAGCGCCCG  
CCATGACACGCTGCCCGTGCCCTAGCAGGAGCCCTGGTGCTACCCCTGTGAAGAGCCAAGCAGCAGGGCACGC  
CTGGCTTTCTTTGGATACCCACTGTCACTGCACTATGAAGTGTGCTGGCTGGGCTTGGTGCTCAGAACAAAG  
CACTGTCACTGCCCACCTCCTTGGGCCTCCTGGAACGCCAGGGCCTCGGCGGCTGCTGAAGGGATTCTATGGCTC  
AGAGGCCCAGGGTGTGGTGAAGGACCTGGAGCCGGAACCTGCTGCGGCACCTGGCAAAAGGCATGGCCTCCCTGAT  
GATCACCACCAAGGGTAGCCCCAGAGGGGAGCTCCGAGGGCAGGTGCACATAGCCAACCAATGTGAGGTTGGCGG  
ACTGCGCCTGGAGGCGGCCGGGGCCGAGGGGGTGCGGGCGCTGGGGGCTCCGGATACAGCCTCTGCTGCGCCGCC  
TGTGGTGCCTGGTCTCCCGGCCCTAGCGCCCGCAAACCTGGTGGTCTTGGGCGGCCCCGAGACCCCAACACATG  
CTTCTTCGAGGGGCAGCAGCGCCCCCACGGGGCTCGCTGGGCGCCCAACTACGACCCGCTCTGCTCACTCTGCAC  
CTGCCAGAGACGAACGGTGATCTGTGACCCGGTGGTGTGCCACCAGCCAGCTGCCCCACACCCGGTGCCAGGCTCC  
CGACCAGTGCTGCCCTGTTTGCCCTGAGAAAACAAGATGTACAGAGACTTGCCAGGGCTGCCAAGGAGCCGGGACCC  
AGGAGAGGGGCTGCTATTTTGATGGTGACCGGAGCTGGCGGGCAGCGGGTACGCGGTGGCACCCCGTTGTGCCCCC  
CTTTGGCTTAATTAAGTGTGCTGTCTGCACCTGCAAGGGGGGCACCTGGAGAGGTGCACTGTGAGAAGGTGCAGTG  
TCCCCGGCTGGCCTGTGCCAGCCTGTGCGTGTCAACCCACCGACTGCTGCAACAGTGTCCAGTGGGGTCGGG  
GGCCCACCCCACTGGGGGACCCCATGCAGGCTGATGGGCCCCGGGGCTGCCGTTTGTGTTGGGCACTGGTTCCC  
AGAGAGTCAGAGCTGGCACCCCTCAGTGCCCCCTTTTGAGAGATGAGCTGTATCACTGCAGATGTGGGGCAGG  
GGTGCCCTCACTGTGAGCGGGATGACTGTTCACTGCCACTGTCTGTGGCTCGGGGAAGGAGAGTCGATGCTGTTT  
CCGCTGCACGGCCCCACCGCGGCCCCCCAGAGACCAGAACTGATCCAGAGCTGGAGAAAGAAGCCGAAGGCTCTTTA  
GGGAGCAGCCAGAGGGCCAAAGTGACCAAGAGGATGGGGCTGAGCTGGGGAAGGGGTGGCATCGAGGACCTTCTT  
GCATTCTCCTGTGGGAAGCCAGTGCCCTTTGCTCCTCTGCTCCTACTCCCCCACTACCTCTGGGAA  
CCACAGCTCCACAAGGGGGAGGAGCAGCTGGGCGCAGACCGAGGTCAAGCCACTCCAAGTCTGCCCTGCCACCC  
TCGGCCTCTGTCTGGAAGCCCCACCCCTTTCTCTGTACATAATGTCACTGGCTTGTGGGATTTTAAATTTA  
TCTTCACTCAGCACCAAGGGCCCCCGACACTCCACTCCTGCTGCCCTGAGCTGAGCAGAGTCATTATTGGAGAG  
TTTTGTATTTATTAAACATTTCTTTTTTCAGTCAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

0944341 = 0831031

><MW: 101960, pI: 8.21, NX(S/T): 5

Signal sequence.

N-glycosylation sites.

**Tyrosine kinase phosphorylation sites.**

N-myristoylation sites.

Amidation site.

Cell attachment sequence.

Leucine zipper pattern.

amino acids 315-337

[illegible]

GGCGGAGCAGCCCTTAGCCGCGCACCGTCTCTCGAGCTCTCGTCGCCACTGCCACCAGCCGCGCGCTCACTGCG  
TCCTGGCTCCGGCTCCCGCGCCCTCCCGGCCGGCCATGCAGCCCCGCGCGCCAGGCGCCCGGTGCGCAGCTGC  
TGCCCGCGCTGGCCCTGCTGCTGCTGCTGCTCGGAGCGGGGCCCCGAGGCAGCTCCCTGGCCAACCCGGTGGCCG  
CCGCGCCCTTGTCTGCGCCCGGGCCGTGCGCCGCGCAGCCCTGCCGGAATGGGGGTGTGTGCACCTCGCGCCCTG  
AGCCGGACCCGAGCACCCGGCCCCCGCCGGCGAGCCTGGCTACAGCTGCACCTGCCCCGCGGGGATCTCCGGCG  
CCAACTGCCAGCTTGTTCAGATCCTTGTGCCAGCAACCCTTGTACCATTGGCAACTGCAGCAGCAGCAGCAGCA  
GCAGCAGCGATGGCTACCTCTGCATTTGCAATGAAGGCTATGAAGGTCCCAACTGTGAACAGGCACTTCCAGTG  
TCCCAGCCACTGGCTGGACCGAATCCATGGCACCCCGACAGCTTCAGCCTGTTTCTGCTACTCAGGAGCCTGACA  
AAATCCTGCCTCGCTCTCAGGCAACGGTGACACTGCCTACCTGGCAGCCGAAAAACAGGGCAGAAAGTTGTAGAAA  
TGAAATGGGATCAAGTGGAGGTGATCCAGATATTGCCCTGTGGGAATGCCAGTTCTAACAGCTCTGCGGGTGGCC  
GCCTGGTATCCTTTGAAGTGCCACAGAACACCTCAGTCAAGATTTCGGCAAGATGCCACTGCCTCACTGATTTTGC  
TCTGGAAGGTACAGGCCACAGGATTCCAACAGTGCTCCCTCATAGATGGACGAAGTGTGACCCCCCTTCAGGCTT  
CAGGGGGACTGGTCCTCCTGGAGGAGATGCTCGCCTTGGGGGAATAATCACTTTATTGGTTTTGTGAATGATTCTG  
TGACTAAGTCTATTGTGGCTTTGCGCTTAACTCTGGTGGTGAAGGTCAGCACCTGTGTGCCGGGGGAGAGTCACG  
CAAATGACTTGGAGTGTTCAGGAAAAGGAAAATGCACCACGAAGCCGTAGAGGCAACTTTTTCTGTACCTGTG  
AGGAGCAGTACGTGGGTACTTTCTGTGAAGAATACGATGCTTGCCAGAGGAAACCTTGCCAAAACAACGCGAGCT  
GTATTGATGCAAATGAAAAGCAAGATGGGAGCAATTTACCCTGTGTTTGCCTTCTGGTTATACTGGAGAGCTTT  
GCCAGTCCAAGATTGATTACTGCATCTTAGACCCATGCAGAAATGGAGCAACATGCATTTCCAGTCTCAGTGGAT  
TCACCTGCCAGTGTCCAGAAGGATATCTCGGATCTGCTTGTGAAGAAAGGTGAGCCCTCGCCCTCGTCTCCGT  
CCGAGAACAACGCGCACCTGTCTATGTGACGGGGTACACTTTACCTGCAACTGCAGCCCGGGCTTCACAGGGCCGA  
CCTGTGCCCAGCTTATTGACTTCTGTGCCCTCAGCCCTGTGCTCATGGCACGTGCCGAGCGTGGGCACCAGCT  
ACAAATGCCTCTGTGATCCAGGTTACCATTGGCCTCTACTGTGAGGAGGAATATAATGAGTGCCTCTCCGCTCCAT  
GCCTGAATGCAGCCACCTGCAGGGACCTCGTTAATGGCTATGAGTGTGTGTGCCTGGCAGAATACAAAGGAACAC  
ACTGTGAATTGTACAAGGATCCCTGCGCTAACGTCAGCTGTCTGAACGGAGCCACCTGTGACAGCGACGGCCTGA  
ATGGCACGTGCATCTGTGCACCCGGGTTTACAGGTGAAGAGTGCACATTGACATAAATGAATGTGACAGTAACC  
CTGCCACCATGGTGGGAGCTGCCTGGACCAGCCCAATGGTTATAACTGCCACTGCCCGCATGGTTGGGTGGGAG  
CAAATGTGAGATCCACCTCCAATGGAAGTCCGGGCACATGGCGGAGAGCCTCACCAACATGCCACGGCACTCCC  
TCTACATCATCATTGGAGCCCTCTGCGTGGCCTTCATCCTTATGCTGATCATCCTGATCGTGGGGATTGCCGCA  
TCAGCCGCATTGAATACCAGGGTTCTTCCAGGCCAGCCTATGAGGAGTTCTACAACCTGCCGAGCATCGACAGCG  
AGTTCAGCAATGCCATTGCATCCATCCGGCATGCCAGGTTTGGAAAGAAATCCCGGCCTGCAATGTATGATGTGA  
GCCCCATCGCCTATGAAGATTACAGTCTGTATGACAAACCCTTGGTCACACTGATTA AAACTAAAGATTTGTAAT  
CTTTTTTTGGATTATTTTTTCAAAAAGATGAGATACTACACTCATTTAATATTTTTTAAGAAAATAAAAAGCTTAA  
GAAATTTAAATGCTAGCTGCTCAAGAGTTTTTCAGTAGAATATTTAAGAACTAATTTTTCTGCAGCTTTTAGTTTTG  
GAAAAATATTTTTAAAAACAAAATTTGTGAAACCTATAGACGATGTTTTAATGTACCTTCAGCTCTCTAAACTGT  
GTGCTTCTACTAGTGTGTGCTCTTTTCACTGTAGACACTATCACGAGACCCAGATTAATTTCTGTGGTTGTTTACA  
GAATAAGTCTAATCAAGGAGAAGTTTCTGTTTGACGTTTGAGTGCCGGCTTTCTGAGTAGAGTTAGGAAAACCAC  
GTAACGTAGCATATGATGTATAATAGAGTATACCCGTTACTTAAAAAGAAGTCTGAAATGTTTCGTTTTGTGGAA  
AGAACTAGTTAAATTTACTATTCCTAACCCGAATGAAATTAGCCTTTGCCTTATTCTGTGCATGGGTAAGTAAC  
TTATTTCTGCAGCTGTTTTGTGTAACCTTTGTGGAAACATTTCTTCGAGTTTGTTTTTGTCACTTTTCGTAACAGTCG  
TCGAATCTAGGCCCTCAAAAACATACGTAACGAAAAGGCCCTAGCGAGGCAAAATTTCTGATTGATTGAACTATATTT  
TTCTTTAAAAAGTCAAGGGTTCTATATTGTAGTAAATTAATTTACATTTGAGTTGTTTGTGTGACTAAGAGGTAG  
TAAATGTAAGAGAGTACTGGTTTCTTCCAGTAGTATGAGTATTTCTCATAGTGCAGCTTTATTTATCTCCAGGATGTT  
TTTGTGGCTGTATTTGATTGATATGTGCTTCTTCTGATTCTTGCTAATTTCCAACCATATTGAATAAATGTGATC  
AAGTCA

## **FIGURE 6**

><subunit 1 of 1, 737 aa, 1 stop

><MW: 78475, pI: 5.09, NX(S/T): 11

MQPRRAQAPGAQLLPALALLLLLLGAGPRGSSLANPVPAAPLSAPGPCAAQPCRNNGGVCTSR  
PEPDPQHPAPAGEPGYSCTCPAGISGANQQLVADPCASNPCHHGNCSSSSSSSSSDGYLCICN  
EGYEGPNCEQALPSLPATGWTESMAPRQLQVPATQEPDKILPRSQATVTLPTWQPKTGQKV  
VEMKWDQVEVIPDIACGNASSNSSAGGRLVSFEVPQNTSVKIRQDATASLILLWKVTATGFQ  
QCSLIDGRSVTPLQASGGLVLLLEMLALGNNHFIGFVNDSVTKSIVALRLTLVVKVSTCVPG  
ESHANDLECSGKGKCTTKPSEATFSC TCEEQYVGTFCEEYDACQRKPCQNNASCIDANEKQD  
GSNFTCVCLPGYTGELCQSKIDYCILDPCRNGATCISSLSGFTCQCPEGYFGSACEEKVDPC  
ASSPCQNNGTCTYVDGVHFTCNCSPGFTGPTCAQLIDFCALSPCAHGTCTRSVGTSTYKCLCDPG  
YHGLYCEEEYNECLSAFCLNAAATCRDLVNGYECVCLA EYKGT HCELYKDPCANVSC L NGATC  
DSDGLNGTICAPGFTGEECDIDINECDSNPCHHGGSCLDQPNGYNCHCPHGWVGANCEIHL  
QWKS GHMAESLTNMPRHS LYIIIGALCVAFILMLIILIVGICRISR IEYQGSSRPAYEEFY N  
CRSIDSEFSNAIASIRHARFGKSRPAMYDVSP IAYEDYSPDDKPLVTLIKTKDL

### **Signal sequence.**

amino acids 1-28

### **Transmembrane domain.**

amino acids 641-660

### **N-glycosylation sites.**

amino acids 107-111, 204-208, 208-212, 223-227, 286-290, 361-365,  
375-379, 442-446, 549-553, 564-568

### **Glycosaminoglycan attachment site.**

amino acids 320-324

### **Tyrosine kinase phosphorylation sites.**

amino acids 490-498, 674-682

### **N-myristoylation sites.**

amino acids 30-36, 56-62, 57-63, 85-91, 106-112, 203-209,  
373-379, 449-455, 480-486, 562-568, 565-571

### **Amidation site.**

amino acids 702-706

### **Aspartic acid and asparagine hydroxylation site.**

amino acids 520-532, 596-608

### **EGF-like domain cysteine pattern signatures.**

amino acids 80-92, 121-133, 336-348, 378-390, 416-428, 454-466,  
491-503, 529-541, 567-579, 605-617

TOEBO" 44644660

## FIGURE 7

CTCTGGAAGGTCACGGCCACAGGATTCCAACAGTGCTCCCTCATAGATGGACGAAAGTGTGA  
CCCCCCTTTCAGGCTTTCAGGGGGACTGGTCCTCCTGGAGGAGATGCTCGCCTTGGGGAATA  
ATCACTTTATTGGTTTTGTGAATGATTCTGTGACTAAGTCTATTGTGGCTTTGCGCTTAAC  
CTGGTGGTGAAGGTCAGCACCTGTGTGCCGGGGGAGAGTCACGCAAATGACTTGGAGTGTT  
AGGAAAAGGAAAATGCACCACGAAGCCGTCAGAGGCAACTTTTTCCTGTACCTGTGAGGAGC  
AGTACGTGGGTACTTTCTGTGAAGAATACGATGCTTGCCAGAGGAAACCTTGCCAAAACAAC  
GCGAGCTGTATTGATGCAAATGAAAAGCAAGATGGGAGCAATTTACCTGTGTTTGCCTTCC  
TGGTTATACTGGAGAGCTTTGCCAACC GA ACTGAGATTGGAGCGAACGACCTACACCGAACT  
GAGATAGGGGAG

094444 08310  
TCTE80" 44644660

## FIGURE 8

CTCTGGAAGGTCACGGCCACAGGATTCCAACAGTGCTCCCTCATAGATGGACGAAAGTGTGA  
CCCCCCTTTTCAGGCTTTTCAGGGGGACTGGTCCTCCTGGAGGAGATGCTCGCCTTGGGGAATA  
ATCACTTTATTGGTTTTGTGAATGATTCTGTGACTAAGTCTATTGTGGCTTTGCGCTTAAC  
CTGGTGGTGAAGGTCAGCACCTGTGTGCCGGGGGAGAGTCACGCAAATGACTTGGAGTGTT  
AGGAAAAGGAAAATGCACCACGAAGCCGTCAGAGGCAACTTTTTCTGTACCTGTGAGGAGC  
AGTACGTGGGTACTTTCTGTGAAGAATACGATGCTTGCCAGAGGAAACCTTGCCAAAACAAC  
GCGAGCTGTATTGATGCAAATGAAAAGCAAGATGGGAGCAATTTACCTGTGTTTGCCTTCC  
TGGTTATACTGGAGAGCTTTGCCAACCGAACTGAGATTGGAGCGAACGACCTACACCGAACT  
GAGATAGGGGAG

0544046460



## FIGURE 9

GCTGAGTCTGCTGCTCCTGCTGCTGCTGCTGCTCCAGCCTGTAACCTGTGCCTACACCACGCCAG  
GCCCCCCCAGAGCCCTCACCACGCTGGGCGCCCCAGAGCCCACACCATGCCGGGCACCTAC  
GCTCCCTCGACCACACTCAGTAGTCCCAGCACCCAGGGCCTGCAAGAGCAGGCACGGGCCCT  
GATGCGGGACTTCCCGCTCGTGACGGCCACAACGACCTGCCCTGGTCCTAAGGCAGGTTT  
ACCAGAAAGGGCTACAGGATGTTAACCTGCGCAATTTAGCTACGGCCAGACCAGCCTGGAC  
AGGCTTAGAGATGGCCTCGTGGGCGCCCAGTTCTGGTCAGCCTATGTGCCATGCCAGACCCA  
GGACCGGGATGCCCTGCGCCTCACCTGGAGCAGATTGACCTCATACGCCGCATGTGTGCCT  
CCTATTCTGAGCTGGAGCTTGTGACCTCGGCTAAAGCTCTGAACGACACTCAGAAATTGGCC  
TGCTCATCGGTGTAGAGGGTGGCCACTCGCTGGACAATAGCCTCTCCATCTTACGTACCTT  
CTACATGCTGGGAGTTCGCTACCTGACGCTCACCCACACCTGCAACACACCCTGGGCAGAGA  
GCTCCGCTAAGGGCGTCCACTCCTTCTACAACAACATCAGCGGGCTGACTGACTTTGGTGAG  
AAGGTGGTGGCAGAAATGAACCGCCTGGGCATGATGGTAGACTTATCCCATGTCTCAGATGC  
TGTGGCACGGCGGGCCCTGGAAGTGTACAGGCACCTGTGATCTTCTCCCACTCGGCTGCCC  
GGGGTGTGTGCAACAGTGCTCGGAATGTTCTGATGACATCCTGCAGCTTCTGAAGAAGAAC  
GGTGGCGTCGTGATGGTGTCTTTGTCCATGGGAGTAATACAGTGCAACCCATCAGCCAATGT  
GTCCACTGTGGCAGATCACTTCGACCACATCAAGGCTGTCATTGGATCCAAGTTCATCGGGA  
TTGGTGGAGATTATGATGGGGCCGGCAAATTCCTCAGGGGCTGGAAGACGTGTCCACATAC  
CCGGTCCTGATAGAGGAGTTGCTGAGTCGTGGCTGGAGTGAGGAAGAGCTTCAGGGTGTCTT  
TCGTGGAAACCTGCTGCGGGTCTTCAGACAAGTGGAAGGTACAGGAAGAAAACAAATGGC  
AAAGCCCCCTGGAGGACAAGTTCCCGGATGAGCAGCTGAGCAGTTCTGCCACTCCGACCTC  
TCACGTCTGCGTCAGAGACAGAGTCTGACTTCAGGCCAGGAACCTCACTGAGATTCCCATACA  
CTGGACAGCCAAGTTACCAGCCAAGTGGTCAGTCTCAGAGTCCTCCCCCACATGGCCCCAG  
TCCTTGCAGTTGTGGCCACCTTCCCAGTCCTTATTCTGTGGCTCTGATGACCCAGTTAGTCC  
TGCCAGATGTCACTGTAGCAAGCCACAGACACCCACAAAGTTCCCCTGTTGTGCAGGCACA  
AATATTTCTGAAATAAATGTTTTGGACATAG

## **FIGURE 10**

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA35595.

<subunit 1 of 1, 433 aa, 1 stop

<MW: 47787, pI: 6.11, NX(S/T): 5

MPGTYAPSTTLSSPSTQGLQEQAARALMRDFPLVDGHNDLPLVLRQVYQKGLQDVNLRNFSYG  
QTSLDRLRDGLVGAQFWSAYVPCQTQDRDALRLTLEQIDLIRMCASYSELELVTSAKALND  
TQKLACLIGVEGGHSLDNSLSILRTFYMLGVRYLTLTHTCNTPWAESSAKGVHSFYNNISGL  
TDFGEKVVAEMNRLGMMVDLSHVSDAVARRALEVSQAPVIFSHSAARGVCNSARNVPDDILQ  
LLKKNNGGVVMVSLSMGVIQCNPANVSTVADHFDHIKAVIGSKFIGIGGDYDGAGKFPQGLE  
DVSTYPVLIEELLSRGWSEELQGVLRGNLLRVFRQVEKVQEENKWQSPLEDKFPDEQLSSS  
CHSDLSRLRQRQSLTSGQELTEIPIHWTAKLPAKWSVSESSPHMAPVLAVVATFPVLILWL

### **N-glycosylation sites.**

amino acids 58-62, 123-127, 182-186, 273-277

### **N-myristoylation sites.**

amino acids 72-78, 133-139, 234-240, 264-270, 334-340, 389-395

### **Renal dipeptidase active site.**

amino acids 134-157

## FIGURE 11

AAAACCTATAAATATTCCGGATTATTCATACCGTCCCACCATCGGGCGCGGATCCGCGGCCG  
CGAATTCTAAACCAACATGCCGGGCACCTACGCTCCCTCGACCACACTCAGTAGTCCCAGCA  
CCCAGGGCCTGCAAGAGCAGGCACGGGCCCTGATGCGGGACTTCCCGCTCGTGGACGGCCAC  
AACGACCTGCCCCTGGTCCTAAGGCAGGTTTACCAGAAAGGGCTACAGGATGTTAACCTGCG  
CAATTTACAGCTACGGCCAGACCAGCCTGGACAGGCTTAGAGATGGCCTCGTGGGCGCCCAGT  
TCTGGTCAGCCTATGTGCCATGCCAGACCCAGGACCGGGATGCCCTGCGCCTCACCTGGAG  
CAGATTGACCTCATACGCCGCATGTGTGCCTCCTATTCTGAGCTGGAGCTTGTGACCTCGGC  
TAAAGCTCTGAACGACACTCAGAAATTGGCCTGCCTCATCGGTGTAGAGGGTGGCCACTCGC  
TGGACAATAGCCTCTCCATCTTACGTACCTTCTACATGCTGGGAGTGCCTACCTGACGCTC  
ACCCACACCTGCAACACACCCTGGGCAGAGAGCTCCGCTAAGGGCGTCCACTCCTTCTACAA  
CAACATCAGCGGGCTGACTGACTTTGGTGAGAAGGTGGTGGCAGAAATGAACCGCCTGGGCA  
TGATGGTAGACTTATCCCATGTCTCAGATGCTGTGGCACGGCGGGCCCTGGAAGTGTACAG  
GCACCTGTGATCTTCTCCCACTCGGCTGCCCCGGGGTGTGTGCAACAGTGCTCGGAATGTTCC  
TGATGACATCCTGCAGCTTCTGAAGAAGAACGGTGGCGTCGTGATGGTGTCTTTGTCCATGG  
GAGTAATACAGTGCAACCCATCAGCCAATGTGTCCACTGTGGCAGATCACTTCGACCACATC  
AAGGCTGTCATTGGATCCAAGTTCATCGGGATTGGTGGAGATTATGATGGGGCCGGCAAATT  
CCCTCAGGGGGCTGGAAGACGTGTCCACATACCCGGTCCTGATAGAGGAGTTGCTGAGTCGTG  
GCTGGAGTGAGGAAGAGCTTCAGGGTGTCTTCGTGGAAACCTGCTGCGGGTCTTCAGACAA  
GTGGAAAAGGTACAGGAAGAAAACAAATGGCAAAGCCCCTTGGAGGACAAGTTCCTCGGATGA  
GCAGCTGAGCAGTTCCTGCCACTCCGACCTCTCACGTCTGCGTCAGAGACAGAGTCTGACTT  
CAGGCCAGGAACTCACTGAGATTCCCATACTGGACAGCCAAGTTACCAGCCAAGTGGTCA  
GTCTCAGAGTCCTCCCCCACCCTGACAAAACCTCACACATGCCACCGTGCCACGACCTGA  
ACTCCTGGGGGGACCGTCAGTCTTCCTCTTCCCCCAAACCCAAGGACACC

0944944-083404

## **FIGURE 12**

></usr/seqdb2/sst/DNA/Dnaseqs.full/ss.DNA35872

><subunit 1 of 1, 446 aa, 0 stop

><NX(S/T): 5

MPGTYAPSTTLSSPSTQGLQEQARALMRDFPLVDGHNDLPLVLRQVYQKGLQDVNLRNFSYG  
QTSLDRLRDGLVGAQFWSAYVPCQTQDRDALRLTLEQIDLIIRMCASYSELELVTSAKALND  
TQKLACLIGVEGGHSLDNSLSILRTFYMLGVRYLTLTHTCNTPWAESSAKGVHSFYNNISGL  
TDFGEKVVAEMNRLGMMVDLSHVSDAVARRALEVSQAPVIFSHSAARGVCNSARNVPDDILQ  
LLKKNNGVVMVSLSMGVIQCNPANVSTVADHFDHIKAVIGSKFIGIGGDYDGAGKFPQGLE  
DVSTYPVLIEELLSRGWSEEELQGVLRGNLLRVFRQVEKVQEENKWQSPLEDKFPDEQLSSS  
CHSDLSRLRQRQSLTSGQELTEIPIHWTAKLPAKWSVSESSPHDPKTHTCPPCPAPELLGGP  
SVFLFPPKPKDT

099444-083101  
T0T280"44544560

## FIGURE 13

CGCCCAGCGACGTGCGGGCGGCCTGGCCCCGCGCCCTCCCGCGCCCGGCCTGCGTCCCGCGCC  
CTGCGCCACCGCCGCGCGAGCCGCAGCCCGCCGCGCGCCCCCGGCAGCGCCGGCCCCATGCCC  
GCCGGCCGCGGGGCCCCGCGCCCAATCCGCGCGGCGGCCGCGCCGTTGCTGCCCCCTGCT  
GCTGCTGCTCTGCGTCCTCGGGGCGCCGCGAGCCGGATCAGGAGCCCACACAGCTGTGATCA  
GTCCCAGGATCCCACGCTTCTCATCGGCTCCTCCCTGCTGGCCACCTGCTCAGTGCACGGA  
GACCCACCAGGAGCCACCGCCGAGGGCCTCTACTGGACCCTCAACGGGCGCCGCCTGCCCCC  
TGAGCTCTCCCGTGTACTCAACGCCTCCACCTTGGCTCTGGCCCTGGCCAACCTCAATGGGT  
CCAGGCAGCGGTGCGGGGACAACCTCGTGTGCCACGCCCCGTGACGGCAGCATCCTGGCTGGC  
TCCTGCCTCTATGTTGGCCTGCCCCCAGAGAAACCCGTCAACATCAGCTGCTGGTCCAAGAA  
CATGAAGGACTTGACCTGCCGCTGGACGCCAGGGGCCCACGGGGAGACCTTCCTCCACACCA  
ACTACTCCCTCAAGTACAAGCTTAGGTGGTATGGCCAGGACAACACATGTGAGGAGTACCAC  
ACAGTGGGGCCCCACTCCTGCCACATCCCCAAGGACCTGGCTCTCTTTACGCCCTATGAGAT  
CTGGGTGGAGGCCACCAACCGCCTGGGCTCTGCCCGCTCCGATGTACTCACGCTGGATATCC  
TGGATGTGGTGACCACGGACCCCCCGCCCGACGTGCACGTGAGCCGCGTCGGGGGCCTGGAG  
GACCAGCTGAGCGTGCGCTGGGTGTCGCCACCCGCCCTCAAGGATTTCTCTTTCAAGCCAA  
ATACCAGATCCGCTACCGAGTGAGGACAGTGTGGACTGGAAGGTGGTGGACGATGTGAGCA  
ACCAGACCTCCTGCCGCCTGGCCGGCCTGAAACCCGGCACCGTGTACTTCGTGCAAGTGCGC  
TGCAACCCCTTTGGCATCTATGGCTCCAAGAAAGCCGGGATCTGGAGTGAGTGGAGCCACCC  
CACAGCCGCCTCCACTCCCCGAGTGAGCGCCCGGGCCCCGGGCGGGGCGTGCGAACCGC  
GGGGCGGAGAGCCGAGCTCGGGGCCGGTGCGGCGCGAGCTCAAGCAGTTCCTGGGCTGGCTC  
AAGAAGCACGCGTACTGCTCCAACCTCAGCTTCGCGCTCTACGACCAGTGGCGAGCCTGGAT  
GCAGAAGTCGCACAAGACCCGCAACCAGGACGAGGGGATCCTGCCCTCGGGCAGACGGGGCA  
CGGCGAGAGGTCCTGCCAGATTAAGCTGTAGGGGCTCAGGCCACCCTCCCTGCCACGTGGAGA  
CGCAGAGGCCGAACCCAAACTGGGGCCACCTCTGTACCCTCACTTCAGGGCACCTGAGCCAC  
CCTCAGCAGGAGCTGGGGTGGCCCCCTGAGCTCCAACGGCCATAACAGCTCTGACTCCACGT  
GAGGCCACCTTTGGGTGCACCCCACTGGGTGTGTGTGTGTGTGTGAGGGTTGGTTGAGTTGC  
CTAGAACCCCTGCCAGGGCTGGGGGTGAGAAGGGGAGTCATTACTCCCCATTACCTAGGGCC  
CCTCCAAAAGAGTCCTTTTAAATAAATGAGCTATTTAGGTGCTGTGATTGTGAAAAAAAAA  
AAA

0944941 "083401"

**THE UNIVERSITY OF CHICAGO**

MPAGRRGPAAQSARRPPPLLPLLLLLLCVLGAPRAGSGAHTAVIS PQDPTLLIGSSLLATCSV  
HGDPPGATAEGLYWTLNGRRLPPELSRVLNASTLALALANLNGSRQRSGDNLVCHARDGSIL  
AGSCLYVGLPPEKPVNISCWSKNMKDLTCRWTPGAHGETFLHTNYS LKYKLRWYGQDNTCEE  
YHTVGPHSCHIPKDLALFTPYEIWVEATNRLGSARSDVLTLDIILDVVTDDPPP DVHVS RVGG  
LEDQLSVRWVSPPALKDFLFQAKYQIRYRVEDSVDWKVVDVSNQTS CRLAGLKPGTVYFVQ  
VRCNPFGIYGSKKAGIWSEWSHPTAASTPRSERPGPGGGACEPRGGEPSSGPVRRELKQFLG  
WLKKHAYCSNLSFRLYDOWRAWMOKSHKTRNQDEGILPSGRRGTARGPAR

amino acids 1-30

## amino acids 44-61

amino acids 92-96, 104-108, 140-144, 168-172, 292-296, 382-386

## amino acids 413-417

amino acids 30-36, 37-43, 73-79, 121-127, 179-185, 218-224,  
300-306, 317-323, 320-326, 347-353, 355-361, 407-413

amino acids 3-7, 79-83, 411-415

## amino acids 325-331

## FIGURE 15

CCCACGCGTCCGCTGGTGTAGATCGAGCAACCCTCTAAAAGCAGTTTAGAGTGGTAAAAAA  
AAAAAAAACACACCAAACGCTCGCAGCCACAAAAGGGATGAAATTTCTTCTGGACATCCTC  
CTGCTTCTCCCGTTACTGATCGTCTGCTCCCTAGAGTCCTTCGTGAAGCTTTTTATTCTTAA  
GAGGAGAAAATCAGTCACCGGCGAAATCGTGCTGATTACAGGAGCTGGGCATGGAATTGGGA  
GACTGACTGCCTATGAATTTGCTAAACTTAAAAGCAAGCTGGTTCTCTGGGATATAAATAAG  
CATGGACTGGAGGAAACAGCTGCCAAATGCAAGGGACTGGGTGCCAAGGTTTATACCTTTGT  
GGTAGACTGCAGCAACCGAGAAGATATTTACAGCTCTGCAAAGAAGGTGAAGGCAGAAATTG  
GAGATGTTAGTATTTTAGTAAATAATGCTGGTGTAGTCTATACATCAGATTTGTTTGCTACA  
CAAGATCCTCAGATTGAAAAGACTTTTGAAGTTAATGTACTTGCACATTTCTGGACTACAAA  
GGCATTCTTCTGCAATGACGAAGAATAACCATGGCCATATTGTCACTGTGGCTTCGGCAG  
CTGGACATGTCTCGGTCCCCTTCTTACTGGCTTACTGTTCAAGCAAGTTTGCTGCTGTTGGA  
TTTCATAAACTTTGACAGATGAACTGGCTGCCTTACAAATAACTGGAGTCAAAACAACATG  
TCTGTGTCCTAATTTTCGTAAACACTGGCTTCATCAAAAATCCAAGTACAAGTTTGGGACCCA  
CTCTGGAACCTGAGGAAGTGGTAAACAGGCTGATGCATGGGATTCTGACTGAGCAGAAGATG  
ATTTTTATTCCATCTTCTATAGCTTTTTTAACAACATTGGAAAGGATCCTTCCTGAGCGTTT  
CCTGGCAGTTTTAAAACGAAAAATCAGTGTTAAGTTTGATGCAGTTATTGGATATAAAATGA  
AAGCGCAATAAGCACCTAGTTTTCTGAAAACCTGATTTACCAGGTTTAGGTTGATGTCATCTA  
ATAGTGCCAGAATTTTAATGTTTGAACCTTCTGTTTTTTCTAATTATCCCCATTTCTTCAATA  
TCATTTTTTGAGGCTTTGGCAGTCTTCATTTACTACCACTTGTTCTTTAGCCAAAAGCTGATT  
ACATATGATATAAACAGAGAAATACCTTTAGAGGTGACTTTAAGGAAAATGAAGAAAAAGAA  
CCAAAATGACTTTTATTAAAATAATTTCCAAGATTATTTGTGGCTCACCTGAAGGCTTTGCAA  
AATTTGTACCATAACCGTTTATTTAACATATATTTTTATTTTTTGATTGCACTTAAATTTTGT  
ATAATTTGTGTTTCTTTTTCTGTTCTACATAAAATCAGAACTTCAAGCTCTCTAAATAAAA  
TGAAGGACTATATCTAGTGGTATTTTACAATGAATATCATGAACTCTCAATGGGTAGGTTTC  
ATCCTACCCATTGCCACTCTGTTTCCTGAGAGATACCTCACATTCCAATGCCAAACATTTCT  
GCACAGGGAAGCTAGAGGTGGATACACGTGTTGCAAGTATAAAAGCATCACTGGGATTTAAG  
GAGAATTGAGAGAATGTACCCACAAATGGCAGCAATAATAAATGGATCACACTTAAAAAAA  
AA  
AA

004494-083404

## **FIGURE 16**

</usr/seqdb2/sst/DNA/Dnaseqs.full/ss.DNA34436

<subunit 1 of 1, 300 aa, 1 stop

<MW: 32964, pI: 9.52, NX(S/T): 1

MKFLLDILLLLPLLLIVCSLESFVKLFIPKRRKSVTGEIVLITGAGHGIGRLTAYEFAKLKSK  
LVLWDINKHGLEETAACKCKGLGAKVHTFVVDCSNREDIYSSAKKVKAIEIGDVSILVNNAGVV  
YTSDLFATQDPQIEKTFEVNVLAHFWTTKAFLPAMTKNNHGHIVTVASAAGHVSVPFLLAYC  
SSKFAAVGFHKTLTDELAALQITGVKTTCLCPNFVNTGFIKNPSTSLGPTLEPEEVNRLMH  
GILTEQKMIFIPSSIAFLTTLERILPERFLAVLKRKISVKFDAVIGYKMKAQ

### **Signal sequence.**

amino acids 1-19

### **Transmembrane domain.**

amino acids 170-187

### **cAMP- and cGMP-dependent protein kinase phosphorylation sites.**

amino acids 30-34, 283-287

### **N-myristoylation sites.**

amino acids 43-49, 72-78, 122-128, 210-216

094494-0310  
T07E80-4464460



## FIGURE 17

GACTAGTTCTCTTGGAGTCTGGGAGGAGGAAAGCGGAGCCGGCAGGGAGCGAACCAGGACTG  
GGGTGACGGCAGGGCAGGGGGCGCCTGGCCGGGGAGAAGCGCGGGGGCTGGAGCACCACCAA  
CTGGAGGGTCCGGAGTAGCGAGCGCCCCGAAGGAGGCCATCGGGGAGCCGGGAGGGGGGACT  
GCGAGAGGACCCCGGCGTCCGGGCTCCCGGTGCCAGCGCTATGAGGCCACTCCTCGTCCTGC  
TGCTCCTGGGCCTGGCGGCCGGCTCGCCCCACTGGACGACAACAAGATCCCCAGCCTCTGC  
CCGGGGCACCCCGGCCTTCCAGGCACGCCGGGCCACCATGGCAGCCAGGGCTTGCCGGGGCCG  
CGATGGCCGCGACGGCCGCGACGGCGCGCCCGGGGCTCCGGGAGAGAAAGGCGAGGGCGGGA  
GGCCGGGACTGCCGGGACCTCGAGGGGACCCCGGGCCGCGAGGAGAGGCGGGACCCGCGGGG  
CCCACCGGGCCTGCCGGGGAGTGCTCGGTGCCTCCGCGATCCGCCTTCAGCGCCAAGCGCTC  
CGAGAGCCGGGTGCCTCCGCCGTCTGACGCACCCTTGCCCTTCGACCGCGTGCTGGTGAACG  
AGCAGGGACATTACGACGCCGTCAACGGCAAGTTCACCTGCCAGGTGCCTGGGGTCTACTAC  
TTCGCCGTCCATGCCACCGTCTACCGGGCCAGCCTGCAGTTTGATCTGGTGAAGAATGGCGA  
ATCCATTGCCTCTTTCTTCCAGTTTTTTCGGGGGGTGGCCCAAGCCAGCCTCGCTCTCGGGGG  
GGGCCATGGTGAGGCTGGAGCCTGAGGACCAAGTGTGGGTGCAGGTGGGTGTGGGTGACTAC  
ATTGGCATCTATGCCAGCATCAAGACAGACAGCACCTTCTCCGGATTTCTGGTGTACTCCGA  
CTGGCACAGCTCCCCAGTCTTTGCTTAGTGCCCACTGCAAAGTGAGCTCATGCTCTCACTCC  
TAGAAGGAGGGTGTGAGGCTGACAACCAGGTCATCCAGGAGGGCTGGCCCCCCTGGAATATT  
GTGAATGACTAGGGAGGTGGGGTAGAGCACTCTCCGTCCTGCTGCTGGCAAGGAATGGGAAC  
AGTGGCTGTCTGCGATCAGGTCTGGCAGCATGGGGCAGTGGCTGGATTTCTGCCCAAGACCA  
GAGGAGTGTGCTGTGCTGGCAAGTGTAAGTCCCCAGTTGCTCTGGTCCAGGAGCCCACGGT  
GGGGTGCTCTCTTCTGCTCCTCTGCTTCTCTGGATCCTCCCCACCCCTCCTGCTCCTGGG  
GCCGGCCCTTTTCTCAGAGATCACTCAATAAACCTAAGAACCCTCATAAAAAAAAAAAAAAAAA  
AAAAAAAAAAAAA

094744-038101

MRPLLVLGLLAAGSPPLDDNKI PSLCPGHPGLPGTPGHHGSQGLPGRDGRDGRDGAPGAP  
GEKGEGGRPGLPGPRGDPGPRGEAGPAGPTGPAGECSVPPRSAFSAKRSESRVPPPSDAPLP  
FDRVLVNEQGHYDAVTGKFTCQVPGVYYFAVHATVYRASLQFDLVKNGESIASFFQFFGGWP  
KPASLSGGAMVRLEPEDOVWVOVGVDYIGIYASIKTDSTFSGFLVYSWDHSSPVFA

amino acids 1-15

amino acids 11-17, 68-74, 216-222

## amino acids 77-80

# FIGURE 19

CTCTTTTGTCCACCAGCCCAGCCTGACTCCTGGAGATTGTGAATAGCTCCATCCAGCCTGAG  
AAACAAGCCGGGTGGCTGAGCCAGGCTGTGCACGGAGCACCTGACGGGCCCCAACAGACCCAT  
GCTGCATCCAGAGACCTCCCCTGGCCGGGGGCATCTCCTGGCTGTGCTCCTGGCCCTCCTTG  
GCACCACCTGGGCAGAGGTGTGGCCACCCCAGCTGCAGGAGCAGGCTCCGATGGCCGGAGCC  
CTGAACAGGAAGGAGAGTTTCTTGCTCCTCTCCCTGCACAACCGCCTGCGCAGCTGGGTCCA  
GCCCCCTGCGGCTGACATGCGGAGGCTGGACTGGAGTGACAGCCTGGCCCCAACTGGCTCAAG  
CCAGGGCAGCCCTCTGTGGAATCCCAACCCCGAGCCTGGCATCCGGCCTGTGGCGCACCCCTG  
CAAGTGGGCTGGAACATGCAGCTGCTGCCCCGCGGGCTTGGCGTCCTTTGTTGAAGTGGTCAG  
CCTATGGTTTGCAGAGGGGCAGCGGTACAGCCACGCGGCAGGAGAGTGTGCTCGCAACGCCA  
CCTGCACCCACTACACGCAGCTCGTGTGGGCCACCTCAAGCCAGCTGGGCTGTGGGCGGCAC  
CTGTGCTCTGCAGGCCAGACAGCGATAGAAGCCTTTGTCTGTGCCTACTCCCCCGGAGGCCAA  
CTGGGAGGTCAACGGGAAGACAATCATCCCCTATAAGAAGGGTGCCTGGTGTTCGCTCTGCA  
CAGCCAGTGTCTCAGGCTGCTTCAAAGCCTGGGACCATGCAGGGGGGCTCTGTGAGGTCCCC  
AGGAATCCTTGTGCGATGAGCTGCCAGAACCATGGACGTCTAACATCAGCACCTGCCACTG  
CCACTGTCCCCCTGGCTACACGGGCAGATACTGCCAAGTGAGGTGCAGCCTGCAGTGTGTGC  
ACGGCCGGTTCCGGGAGGAGGAGTGCTCGTGCGTCTGTGACATCGGCTACGGGGGAGCCCAG  
TGTGCCACCAAGGTGCATTTTCCCTTCCACACCTGTGACCTGAGGATCGACGGAGACTGCTT  
CATGGTGTCTTCAGAGGCAGACACCTATTACAGAGCCAGGATGAAATGTCAGAGGAAAGGCG  
GGGTGCTGGCCCAGATCAAGAGCCAGAAAGTGCAAGGACATCCTCGCCTTCTATCTGGGCCGC  
CTGGAGACCACCAACGAGGTGACTGACAGTGACTTCGAGACCAGGAACTTCTGGATCGGGCT  
CACCTACAAGACCGCCAAGGACTCCTTCCGCTGGGCCACAGGGGAGCACCAGGCCTTACCA  
GTTTTGCCTTTGGGCAGCCTGACAACCACGGGCTGGTGTGGCTGAGTGCTGCCATGGGGTTT  
GGCAACTGCGTGGAGCTGCAGGCTTCAGCTGCCTTCAACTGGAACGACCAGCGCTGCAAAAC  
CCGAAACCGTTACATCTGCCAGTTTGCCCAGGAGCACATCTCCCGGTGGGGCCCAGGGTCCT  
GAGGCCTGACCACATGGCTCCCTCGCCTGCCCTGGGAGCACCGGCTCTGCTTACCTGTCTGC  
CCACCTGTCTGGAACAAGGGCCAGGTTAAGACCACATGCCTCATGTCCAAAGAGGTCTCAGA  
CCTTGACAAATGCCAGAAGTTGGGCAGAGAGAGGCAGGGAGGCCAGTGAGGGCCAGGGAGTG  
AGTGTTAGAAGAAGCTGGGGCCCTTCGCCTGCTTTTGATTGGGAAGATGGGCTTCAATTAGA  
TGGCGAAGGAGAGGACACCGCCAGTGGTCCAAAAGGCTGCTCTCTTCCACCTGGCCCAGAC  
CCTGTGGGGCAGCGGAGCTTCCCTGTGGCATGAACCCACGGGGTATTAAATTATGAATCAG  
CTGAAAAAAAAAAAAA

10780"4464660

## FIGURE 20

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA44176

<subunit 1 of 1, 455 aa, 1 stop

<MW: 50478, pI: 8.44, NX(S/T): 2

MLHPETSPGRGHLLAVLLALLGTTWAEVWPPQLQEQAPMAGALNRKESFLLLSLHNRLRSWV  
QPPAADMRRLDWSDSLAQLAQARAALCGIPTPSLASGLWRTLQVGWNMQLLPAGLASFVEVV  
SLWFAEGQRYSHAAGECARNATCTHYTQLVWATSSQLGCGRHLCSAGQTAIEAFVCAYSPPG  
NWEVNGKTIIPYKKGAWCSLCTASVSGCFKAWDHAGGLCEVPRNPCRMSCQNHGRLNISTCH  
CHCPPGYTGRYCQVRCSLQCVHGRFREEECSCVCDIGYGGAQCATKVHFPFHTCDLRIDGDC  
FMVSSEADTYRARMKQCQRKGGVLAQIKSQKVQDILAFYLGRLTNEVTDSDFETRNF  
WIG  
LTYKTAKDSFRWATGEHQAFSTFAFGQPDNHGLVWLSAAMGFGNCVELQASAAFNWNDQRCK  
TRNRYICQFAQEHISRWGPGS

### **Signal sequence.**

amino acids 1-26

### **Transmembrane domain.**

amino acids 110-124

### **N-glycosylation sites.**

amino acids 144-148, 243-247

### **cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 45-49

### **N-myristoylation sites.**

amino acids 22-28, 99-105, 131-137, 201-207, 213-219, 287-293,  
288-294, 331-337, 398-404

### **Prokaryotic membrane lipoprotein lipid attachment site.**

amino acids 204-215

### **EGF-like domain cysteine pattern signature.**

amino acids 249-261, 280-292

### **C-type lectin domain signature.**

amino acids 417-442

FIGURE 20

060449Z 080310Z

CGGACGCGTGGGCTGGGCGCTGCAAAAGCGTGTCCCGCCGGGTCCCGAGCGTCCCGCGCCCT  
CGCCCCGCCATGCTCCTGCTGCTGGGGCTGTGCCTGGGGCTGTCCCTGTGTGTGGGGTCGCA  
GGAAGAGGCGCAGAGCTGGGGCCACTCTTCGGAGCAGGATGGAATCAGGGTCCCGAGGCAAG  
TCAGACTGTTGCAGAGGCTGAAAACCAAACCTTTGATGACAGAATTCTCAGTGAAGTCTACC  
ATCATTTCCCGTTATGCCTTCACTACGGTTTTCCTGCAGAATGCTGAACAGAGCTTCTGAAGA  
CCAGGACATTGAGTTCAGATGCAGATTCCAGCTGCAGCTTTCATCACCAACTTCACTATGC  
TTATTGGAGACAAGGTGTATCAGGGCGAAATTACAGAGAGAGAAAAGAAGAGTGGTGATAGC  
GTAAAAGAGAGAAAGGAATAAAACCACAGAAGAAAATGGAGAGAAGGGGACTGAAATATTCAG  
AGCTTCTGCAGTGATTCCCAGCAAGGACAAAGCCGCCTTTTTTCCTGAGTTATGAGGAGCTTC  
TGCAGAGGCGCCTGGGCAAGTACGAGCACAGCATCAGCGTGCGGCCCCAGCAGCTGTCCGGG  
AGGCTGAGCGTGGACGTGAATATCCTGGAGAGCGCGGGCATCGCATCCCTGGAGGTGCTGCC  
GCTTCACAACAGCAGGCAGAGGGGCAGTGGGCGCGGGGAAGATGATTCTGGGCCTCCCCAT  
CTACTGTCATTAAACCAAAATGAAACATTTGCCAACATAATTTTAAACCTACTGTAGTACAA  
CAAGCCAGGATTGCCCAGAATGGAATTTTGGGAGACTTTATCATTAGATATGACGTCAATAG  
AGAACAGAGCATTGGGGACATCCAGGTTCTAAATGGCTATTTTGTGCACTACTTTGCTCCTA  
AAGACCTTCCTCCTTTACCCAAGAATGTGGTATTTCGTGCTTGACAGCAGTGCTTCTATGGTG  
GGAACCAAACCTCCGGCAGACCAAGGATGCCCTCTTCACAATTCTCCATGACCTCCGACCCCA  
GGACCGTTTCAGTATCATTGGATTTTCCAACCGGATCAAAGTATGGAAGGACCACCTTGATAT  
CAGTCACTCCAGACAGCATCAGGGATGGGAAAGTGTACATTCAACCATATGTCAACCACTGGA  
GGCACAGACATCAACGGGGGCCCTGCAGAGGGCCATCAGGCTCCTCAACAAGTACGTGGCCCA  
CAGTGGCATTGGAGACCGGAGCGTGTCCCTCATCGTCTTTCCTGACGGATGGGAAGCCACGG  
TCGGGGAGACGCACACCCTCAAGATCCTCAACAACACCCGAGAGGCGCCCGAGGCCAAGTC  
TGCATCTTCACCATTGGCATCGGCAACGACGTGGACTTCAGGCTGCTGGAGAAACTGTGCGT  
GGAGAACTGTGGCCTCACACGGCGCGTGCACGAGGAGGAGGACGCAGGCTCGCAGCTCATCG  
GGTTCTACGATGAAATCAGGACCCCGCTCCTCTCTGACATCCGCATCGATTATCCCCCAGC  
TCAGTGGTGCAGGCCACCAAGACCCTGTTCCCCAACTACTTCAACGGCTCGGAGATCATCAT  
TGCGGGGGAAGCTGGTGGACAGGAAGCTGGATCACCTGCACGTGGAGGTCACCGCCAGCAACA  
GTAAGAAATTTCATCATCCTGAAGACAGATGTGCCTGTGCGGCCTCAGAAGGCAGGGAAAGAT  
GTCACAGGAAGCCCCAGGCCTGGAGGCGATGGAGAGGGGGACACCAACCACATCGAGCGTCT  
CTGGAGCTACCTCACCAACAAAGGAGCTGCTGAGCTCCTGGCTGCAAAGTGACGATGAACCGG  
AGAAGGAGCGGCTGCGGCAGCGGGCCAGGCCCTGGCTGTGAGCTACCGCTTCCTCACTCCC  
TTCACCTCCATGAAGCTGAGGGGGGCCGGTCCCACGCATGGATGGCCTGGAGGAGGCCACGG  
CATGTGCGGCTGCCATGGGACCCGAACCGGTGGTGCAGAGCGTGCAGAGGAGCTGGCACGCAGC  
CAGGACCTTTGCTCAAGAAGCCAAACTCCGTCAAAAAAAAAACAAAACAAAAACAAAAAAAAGA  
CATGGGAGAGATGGTGTTTTTCTCTCCACCACCTGGGGATACGATGAGAAAGATGGCCACCT  
GCAAGCCAGGAAGACGGCCCTCACCAGACACCATGTCTGCTGGCACCTTGATCTTGACCTC  
CCAGCCTCCAGAACTGTGAGAAATAAATGTGTTTTGTTTAAAGCTAAAAAAAAAAAAAAAAAAAA  
AA

**SECRET**

MLLLLGLCLGLSLCVGSQEEAQSWGHSSEQDGLRVPRQVRLLQRLKTKPLMTEFSVKSTIIIS  
RYAFTTVSCRMLNRASEDQDIEFQMQUIPAAAFITNFTMLIGDKVYQGEITEREKKSGDRVKE  
KRNKTTENGINEKGTEIFRASAVIPSKDKAAFFLSYEELLQRRLGKYEHSISVRPQQLSGRLS  
VDVNILESAGIASLEVLPLHNSRQRGSGRGEDDSGPPPSTVINQNETFANIIFKPTVVQQAR  
IAQNGILGDFIIRYDVNREQSIGDIQVLNGYFVHYFAPKDLPLPKNVFVLDSSASMVGTK  
LRQTKDALFTILHDLRPQDRFSIIGFSNRIKVWKDHLISVTPDSIRDGKVYIHHMSPTGGTD  
INGALQRAIRLLNKYVAHSGIGDRSVSLIVFLTDGKPTVGETHTLKI LNNTREAARGQVCIF  
TIGIGNDVDFRLLEKLSLENCGLTRRVHEEEDAGSQLIGFYDEIRTPLLSDIRIDYPPSSVV  
QATKTLFPNYFNGSEII IAGKLVDRLKLDHLHVEVTASNSKKFIILKTDVPVRPQKAGKDV TG  
SPRPGGDGEGDTNHIERLWSYLTTKELLSSWLQSDDEPEKERLRQRAQALAVSYRFLTPTFS  
MKLRGPVPRMDGLEEAHGMSAAMGPEPVVQSVRGAGTQPGPLLKKPNSVKKKQNKTKKRHGR  
DGVFPLHHLGIR

amino acids 1-14

amino acids 97-101, 127-131, 231-235, 421-425, 508-512, 674-678

## amino acids 213-217, 391-395

amino acids 6-12, 10-16, 212-218, 370-376, 632-638, 638-644

## FIGURE 23

CGGACGCGTGGGGTGCCCGACATGGCGAGTGTAGTGCTGCCGAGCGGATCCCAGTGTGCGGC  
GGCAGCGGCGGCGGCGGCGCCTCCCGGGCTCCGGCTTCTGCTGTTGCTCTTCTCCGCCGCGG  
CACTGATCCCCACAGGTGATGGGCAGAATCTGTTTACGAAAGACGTGACAGTGATCGAGGGA  
GAGGTTGCGACCATCAGTTGCCAAGTCAATAAGAGTGACGACTCTGTGATTCAGCTACTGAA  
TCCCAACAGGCAGACCATTTATTTTCAGGGACTTCAGGCCTTTGAAGGACAGCAGGTTTCAGT  
TGCTGAATTTTTCTAGCAGTGAAGTCAAAGTATCATTGACAAACGTCTCAATTTCTGATGAA  
GGAAGATACTTTTGCCAGCTCTATACCGATCCCCACAGGAAAGTTACACCACCATCACAGT  
CCTGGTCCCACCACGTAATCTGATGATCGATATCCAGAAAGACACTGCCGGTGGAAGGTGAGG  
AGATTGAAGTCAACTGCACTGCTATGGCCAGCAAGCCAGCCACGACTATCAGGTGGTTCAAA  
GGGAACACAGAGCTAAAAGGCAAATCGGAGGTGGAAGAGTGGTCAGACATGTACACTGTGAC  
CAGTCAGCTGATGCTGAAGGTGCACAAGGAGGACGATGGGGTCCCAGTGATCTGCCAGGTGG  
AGCACCTGCGGTCACTGGAAACCTGCAGACCCAGCGGTATCTAGAAGTACAGTATAAGCCT  
CAAGTGCACATTCAGATGACTTATCCTCTACAAGGCTTAACCCGGAAGGGGACGCGCTTGA  
GTTAACATGTGAAGCCATCGGGAAGCCCCAGCCTGTGATGGTAACCTGGGTGAGAGTCGATG  
ATGAAATGCCTCAACACGCCGTACTGTCTGGGCCCAACCTGTTCAATAACCTAAACAAA  
ACAGATAATGGTACATACCGCTGTGAAGCTTCAAACATAGTGGGGAAAGCTCACTCGGATTA  
TATGCTGTATGTATACGATCCCCCACAACCTATCCCTCCTCCCACAACAACCACCACCACCA  
CCACCACCACCACCACCACCATCCTTACCATCATCACAGATTCCCGAGCAGGTGAAGAAGGC  
TCGATCAGGGCAGTGGATCATGCCGTGATCGGTGGCGTCGTGGCGGTGGTGGTGTTCGCCAT  
GCTGTGCTTGCTCATCATTCTGGGGCGCTATTTTGCCAGACATAAAGGTACATACTTCACTC  
ATGAAGCCAAAGGAGCCGATGACGCAGCAGACGCAGACACAGCTATAATCAATGCAGAAGGA  
GGACAGAACAACTCCGAAGAAAAGAAAGAGTACTTCATCTAGATCAGCCTTTTTGTTTCAAT  
GAGGTGTCCAACCTGGCCCTATTTAGATGATAAAGAGACAGTGATATTGG

107E80" 4464660

## FIGURE 24

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA39518

<subunit 1 of 1, 440 aa, 1 stop

<MW: 48240, pI: 4.93, NX(S/T): 7

MASVVLPSGSQCAAAAAAAAAAPPGLRLLLLLFSAAALIPTGDGQNLFTKDVTVIEGEVATISC  
QVNKSDDSVIQLLNPNRQTIYFRDFRPLKDSRFQLLNFSSELKVSLTNVSISDEGRYFCQL  
YTDPPQESYTTITVLVPPRNLMDIQKDTAVEGEEIEVNCTAMASKPATTIRWFKGNTELKG  
KSEVEEWSDMYTVTSQMLMLKVHKEDDGVPVICQVEHPAVTGNLQTQRYLEVQYKPQVHIQMT  
YPLQGLTREGDALELTCEAIGKPQPMVMTWVRVDDMPQHAVLSGPNLFINNLNKTNDNGTYR  
CEASNIVGKAHSDYMLYVYDPPTTIPPTTTTTTTTTTTTTTILTIITDSRAGEEGSIRAVDH  
AVIGGVVAVVVFAMLCLLIILGRYFARHKGTYFTHEAKGADDAADADTAIINAEGGQNNSEE  
KKEYFI

### **Signal sequence.**

amino acids 1-36

### **Transmembrane domain.**

amino acids 372-393

### **N-glycosylation sites.**

amino acids 65-69, 99-103, 111-115, 163-167, 302-306, 306-310,  
430-434

### **Tyrosine kinase phosphorylation sites.**

amino acids 233-240, 319-328

### **N-myristoylation sites.**

amino acids 9-15, 227-233, 307-313, 365-371, 376-382, 402-408,  
411-417, 427-433, 428-432

09444083101  
T0T280"44544660



## FIGURE 25

GGGGCGGGTGGACGCGGACTCGAACGCGAGTTGCTTCGGGACCCAGGACCCCTCGGGCCCGA  
CCCGCCAGGAAAGACTGAGGCCGCGGCCTGCCCGCCGGCTCCCTGCGCCGCGCCGCGCCTC  
CCGGGACAGAAGATGTGCTCCAGGGTCCCTCTGCTGCTGCCGCTGCTCCTGCTACTGGCCCT  
GGGGCCTGGGGTGCAGGGCTGCCCATCCGGCTGCCAGTGCAGCCAGCCACAGACAGTCTTCT  
GCACTGCCCCGCCAGGGGACCACGGTGCCCCGAGACGTGCCACCCGACACGGTGGGGCTGTAC  
GTCTTTGAGAACGGCATCACCATGCTCGACGCAAGCAGCTTTGCCGGCCTGCCGGGCCTGCA  
GCTCCTGGACCTGTACAGAACCAGATCGCCAGCCTGCGCCTGCCCCGCTGCTGCTGCTGG  
ACCTCAGCCACAACAGCCTCCTGGCCCTGGAGCCCGGCATCCTGGACACTGCCAACGTGGAG  
GCGCTGCGGCTGGCTGGTCTGGGGCTGCAGCAGCTGGACGAGGGGCTCTTCAGCCGCTTGCG  
CAACCTCCACGACCTGGATGTGTCCGACAACCAGCTGGAGCGAGTGCCACCTGTGATCCGAG  
GCCTCCGGGGCCTGACGCGCCTGCGGCTGGCCGGCAACACCCGCATTGCCCAGCTGCGGGCC  
GAGGACCTGGCCGGCCTGGCTGCCCTGCAGGAGCTGGATGTGAGCAACCTAAGCCTGCAGGC  
CCTGCCTGGCGACCTCTCGGGCCTCTTCCCCCGCCTGCGGCTGCTGGCAGCTGCCCGCAACC  
CCTTCAACTGCGTGTGCCCCCTGAGCTGGTTTGCCCCCTGGGTGCGCGAGAGCCACGTCA  
CTGGCCAGCCCTGAGGAGACGCGCTGCCACTTCCCCGCCAAGAACGCTGGCCGGCTGCTCCT  
GGAGCTTGACTACGCCGACTTTGGCTGCCCAGCCACCACCACACAGCCACAGTGCCCA  
CGAGGCCCCGTGGTGCGGGAGCCACAGCCTTGCTTCTAGCTTGGCTCCTACCTGGCTTAGC  
CCACAGCGCCGGCCACTGAGGCCCCAGCCCGCCCTCCACTGCCCCACCGACTGTAGGGCC  
TGTCCCCCAGCCCCAGGACTGCCACCGTCCACCTGCCTCAATGGGGGCACATGCCACCTGG  
GGACACGGCACCACCTGGCGTGCTTGTCGCCCGAAGGCTTCACGGGCCTGTACTGTGAGAGC  
CAGATGGGGCAGGGGACACGGCCCAGCCCTACACCAGTCACGCCGAGGGCCACCACGGTCCCT  
GACCCTGGGCATCGAGCCGGTGAGCCCCACCTCCCTGCGCGTGGGGCTGCAGCGCTACCTCC  
AGGGGAGCTCCGTGCAGCTCAGGAGCCTCCGTCTCACCTATCGCAACCTATCGGGCCCTGAT  
AAGCGGCTGGTGACGCTGCGACTGCCTGCCTCGCTCGCTGAGTACACGGTCACCCAGCTGCG  
GCCCAACGCCACTTACTCCGTCTGTGTATGCCTTTGGGGCCCCGGGCGGGTGCCGGAGGGCG  
AGGAGGCCTGCGGGGAGGGCCATACACCCCCAGCCGTCCACTCCAACCACGCCCCAGTCACC  
CAGGCCCCGCGAGGGCAACCTGCCGCTCCTCATTGCGCCCCCCTGGCCGCGGTGCTCCTGGC  
CGCGCTGGCTGCGGTGGGGGCAGCCTACTGTGTGCGGCGGGGGCGGGCCATGGCAGCAGCGG  
CTCAGGACAAAGGGCAGGTGGGGCCAGGGGCTGGGGCCCTGGAACCTGGAGGGAGTGAAGGTC  
CCCTTGAGGCCAGGCCCCAAGGCAACAGAGGGCGGTGGAGAGGCCCTGCCCAGCGGGTCTGA  
GTGTGAGGTGCCACTCATGGGCTTCCCAGGGCCTGGCCTCCAGTCACCCCTCCACGCAAAGC  
CCTACATCTAAGCCAGAGAGAGACAGGGCAGCTGGGGCCGGGCTCTCAGCCAGTGAGATGGC  
CAGCCCCCTCCTGCTGCCACACCACGTAAGTTCTCAGTCCCAACCTCGGGGATGTGTGCAGA  
CAGGGCTGTGTGACCACAGCTGGGCCCTGTTCCCTCTGGACCTCGGTCTCCTCATCTGTGAG  
ATGCTGTGGCCCAGCTGACGAGCCCTAACGTCCCCAGAACCGAGTGCTATGAGGACAGTGT  
CCGCCCTGCCCTCCGCAACGTGCAGTCCCTGGGCACGGCGGGCCCTGCCATGTGCTGGTAAC  
GCATGCCTGGGCCCTGCTGGGCTCTCCCACTCCAGGCGGACCCTGGGGGCCAGTGAAGGAAG  
CTCCCGGAAAGAGCAGAGGGAGAGCGGGTAGGCGGCTGTGTGACTCTAGTCTTGGCCCCAGG  
AAGCGAAGGAACAAAAGAACTGGAAAGGAAGATGCTTTAGGAACATGTTTTGCTTTTTTAA  
AATATATATATATTTATAAGAGATCCTTTCCCATTTATTCTGGGAAGATGTTTTTCAAAC  
AGAGACAAGGACTTTGGTTTTTGTAAAGACAAACGATGATATGAAGGCCTTTTGTAAAGAAAA  
ATAAAAAAAAAA

## **FIGURE 26**

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA44804

<subunit 1 of 1, 598 aa, 1 stop

<MW: 63030, pI: 7.24, NX(S/T): 3

MCSRVPLLLPLLLLLLALGPGVQGCPSGCQCSQPQTTFCTARQGTTPRDVPPDTVGLYVFEN  
GITMLDASSFAGLPGLQLLDLSQNQIASLRLPRLLLLDLSHNSLLALEPGIILDTANVEALRL  
AGLGLQQLDEGLFSRLRNLDLDVSDNQLERVPPVIRGLRGLTRLRLAGNTRIAQLRPEDLA  
GLAALQELDVSNLSLQALPGDLSGLFPRLRLAAARNPFNCVPLSWFGPWVRESHVTLASP  
EETRCHFPKKNAGRLLLELDYADFGCPATTTTATVPTTRPVVREPTALSSSLAPTWLSPTAP  
ATEAPSPSTAPPTVGPVPQPDQCPSTCLNGGTCHLGRHHLACLCPEGFTGLYCESQMGQ  
GTRPSPTPVTTPRPPRSLTLGIEPVSPSTSLRVGLQRYLQGSSVQLRSLRLTYRNLSGPDKRLV  
TLRLPASLAEYTVTQLRPNATYSVCVMPLGPGRVPEGEEACGEAHTPPAVHSNHAPVTQARE  
GNLPLLIAPALAAVLLAALAAVGAAYCVRGRAMAAAAQDKGQVGPGAGPLELEGVKVPLEP  
GPKATEGGGEALPSGSECEVPLMGFPGLQSPHAKPYI

**Signal sequence.**

amino acids 1-23

**Transmembrane domain.**

amino acids 501-522

**N-glycosylation sites.**

amino acids 198-202, 425-429, 453-457

**Tyrosine kinase phosphorylation site.**

amino acids 262-270

**N-myristoylation sites.**

amino acids 23-29, 27-33, 112-118, 273-279, 519-525, 565-571

**Prokaryotic membrane lipoprotein lipid attachment site.**

amino acids 14-25

**EGF-like domain cysteine pattern signature.**

amino acids 355-367

**Leucine zipper pattern.**

amino acids 122-144, 194-216

TEEB" 464460

## **FIGURE 27**

GGCACTAGGACAACCTTCTTCCCTTCTGCACCACTGCCCCGTACCCTTACCCGCCCCGCCACC  
TCCTTGCTACCCCACTCTTGAAACCACAGCTGTTGGCAGGGTCCCCAGCTCATGCCAGCCTC  
ATCTCCTTTCTTGCTAGCCCCCAAAGGGCCTCCAGGCAACATGGGGGGCCAGTCAGAGAGC  
CGGCACTCTCAGTTGCCCTCTGGTTGAGTTGGGGGGCAGCTCTGGGGGCCGTGGCTTGTGCC  
ATGGCTCTGCTGACCCAACAAACAGAGCTGCAGAGCCTCAGGAGAGAGGTGAGCCGGCTGCA  
GGGGACAGGAGGCCCCCTCCAGAATGGGGAAGGGTATCCCTGGCAGAGTCTCCCGGAGCAGA  
GTTCCGATGCCCTGGAAGCCTGGGAGAATGGGGAGAGATCCCGGAAAAGGAGAGCAGTGCTC  
ACCCAAAAACAGAAGAAGCAGCACTCTGTCCTGCACCTGGTTCCCATTAACGCCACCTCCAA  
GGATGACTCCGATGTGACAGAGGTGATGTGGCAACCAGCTCTTAGGCGTGGGAGAGGCCTAC  
AGGCCCAAGGATATGGTGTCCGAATCCAGGATGCTGGAGTTTATCTGCTGTATAGCCAGGTC  
CTGTTTCAAGACGTGACTTTCACCATGGGTCAGGTGGTGTCTCGAGAAGGCCAAGGAAGGCA  
GGAGACTCTATTCCGATGTATAAGAAGTATGCCCTCCCACCCGGACCGGGCCTACAACAGCT  
GCTATAGCGCAGGTGTCTTCCATTTACACCAAGGGGATATTCTGAGTGTCATAATTCCCCGG  
GCAAGGGCGAACTTAACCTCTCTCCACATGGAACCTTCCTGGGGTTTGTGAACTGTGAATT  
GTGTTATAAAAAGTGGCTCCCAGCTTGGAAGACCAGGGTGGGTACATACTGGAGACAGCCAA  
GAGCTGAGTATATAAAGGAGAGGGAATGTGCAGGAACAGAGGCATCTTCCTGGGTTTGGCTC  
CCCGTTCCTCACTTTTCCCTTTTCATTCCCACCCCTAGACTTTGATTTTACGGATATCTTG  
CTTCTGTTCCCCATGGAGCTCCG

09440301-45460

**SECRET**

MPASSPFL LAPKGPPGNMGGPVREPALSVALWLSWGAALGAVACAMALLTQQTELQSLRREV  
SRLQGTGGPSQNGEGYPWQSLPEQSSDALEAWENGERSRKRRAVLTQKQKKQHSVLHLVPIN  
ATSKDDSDVTEVMWQPALRRGRGLQAQGYGVR IQDAGVYLLYSQVLFQDVTFTMGQVVSREG  
QGRQETLFR CIRSMPSHPDRAYNSCYSAGVFHLHQGDILSVII PRARAKLNLSPHGTFLGFVKL

amino acids 1-40

amino acids 124-128

## amino acids 156-164

amino acids 36-42, 40-46, 179-185, 242-248

## amino acids 34-45

# FIGURE 29

CACTTTCTCCCTCTCTTCTTTACTTTTCGAGAAACCGCGCTTCCGCTTCTGGTCGCAGAGAC  
CTCGGAGACCGCGCCGGGGAGACGGAGGTGCTGTGGGTGGGGGGACCTGTGGCTGCTCGTA  
CCGCCCCCACCCTCCTCTTCTGCACTGCCGTCTCCGGAAGACCTTTTCCCCTGCTCTGTT  
TCCTTCACCGAGTCTGTGCATCGCCCCGGACCTGGCCGGGAGGAGGCTTGGCCGGCGGGAGA  
TGCTCTAGGGGCGGCGCGGGAGGAGCGGCCGGCGGGACGGAGGGCCCCGGCAGGAAGATGGGC  
TCCCGTGGACAGGGACTCTTGCTGGCGTACTGCCTGCTCCTTGCTTTGCTCTGGCCTGGT  
CCTGAGTCGTGTGCCCCATGTCCAGGGGGAACAGCAGGAGTGGGAGGGGACTGAGGAGCTGC  
CGTCGCCTCCGGACCATGCCGAGAGGGCTGAAGAACAACATGAAAAATACAGGCCCAGTCAG  
GACCAGGGGCTCCCTGCTTCCCGGTGCTTGCGCTGCTGTGACCCCGGTACCTCCATGTACCC  
GGCGACCGCCGTGCCCCAGATCAACATCACTATCTTGAAAGGGGAGAAGGGTGACCGCGGAG  
ATCGAGGCCTCCAAGGGAAATATGGCAAAACAGGCTCAGCAGGGGCCAGGGGCCACACTGGA  
CCCAAAGGGCAGAAGGGCTCCATGGGGGCCCCCTGGGGAGCGGTGCAAGAGCCACTACGCCGC  
CTTTTCGGTGGGCCGGAAGAAGCCCATGCACAGCAACCACTACTACCAGACGGTGATCTTCG  
ACACGGAGTTCGTGAACCTCTACGACCACTTCAACATGTTACCGGCAAGTTCTACTGCTAC  
GTGCCCGGCTCTACTTCTTACGCTCAACGTGCACACCTGGAACCAGAAGGAGACCTACCT  
GCACATCATGAAGAACGAGGAGGAGGTGGTGATCTTGTTGCGCGAGGTGGGCGACCGCAGCA  
TCATGCAAAGCCAGAGCCTGATGCTGGAGCTGCGAGAGCAGGACCAGGTGTGGGTACGCCTC  
TACAAGGGCGAACGTGAGAACGCCATCTTCAGCGAGGAGCTGGACACCTACATCACCTTCAG  
TGGCTACCTGGTCAAGCACGCCACCGAGCCCTAGCTGGCCGGCCACCTCCTTTCTCTCGCC  
ACCTTCCACCCCTGCGCTGTGCTGACCCACCGCCTCTTCCCCGATCCCTGGACTCCGACTC  
CCTGGCTTTGGCATTCACTGAGACGCCCTGCACACACAGAAAGCCAAAGCGATCGGTGCTCC  
CAGATCCCGCAGCCTCTGGAGAGAGCTGACGGCAGATGAAATCACCAGGGCGGGGCACCCGC  
GAGAACCCTCTGGGACCTTCCGCGGCCCTCTCTGCACACATCCTCAAGTGACCCCGCACGGC  
GAGACGCGGGTGGCGGCAGGGCGTCCAGGGTGCGGCACCGCGGCTCCAGTCTTTGGAATA  
ATTAGGCAAATTCTAAAGGTCTCAAAGGAGCAAAGTAAACCGTGGAGGACAAAGAAAAGG  
TTGTTATTTTGTCTTTCCAGCCAGCCTGCTGGCTCCCAAGAGAGAGGCCTTTTCAGTTGAG  
ACTCTGCTTAAGAGAAGATCCAAAGTTAAAGCTCTGGGGTCAGGGGAGGGGCCGGGGCAGG  
AAACTACCTCTGGCTTAATTCTTTTAAGCCACGTAGGAACCTTTCTTGAGGGATAGGTGGACC  
CTGACATCCCTGTGGCCTTGCCCCAAGGGCTCTGCTGGTCTTTCTGAGTCACAGCTGCGAGGT  
GATGGGGGCTGGGGCCCCAGGCGTCAGCCTCCAGAGGGACAGCTGAGCCCCCTGCCTTGGC  
TCCAGGTTGGTAGAAGCAGCCGAAGGGCTCCTGACAGTGGCCAGGGACCCCTGGGTCCCCCA  
GGCCTGCAGATGTTTCTATGAGGGGCAGAGCTCCTTGGTACATCCATGTGTGGCTCTGCTCC  
ACCCCTGTGCCACCCACAGAGCCCTGGGGGGTGGTCTCCATGCCTGCCACCCTGGCATCGGCT  
TTCTGTGCCGCTCCACACAAATCAGCCCCAGAAGGCCCGGGGCTTGGCTTCTGTTTTT  
TATAAAACACCTCAAGCAGCACTGCAGTCTCCCATCTCCTCGTGGGCTAAGCATCACCGCTT  
CCACGTGTGTTGTGTTGGTTGGCAGCAAGGCTGATCCAGACCCCTTCTGCCCCACTGCCCT  
CATCCAGGCCTCTGACCAGTAGCCTGAGAGGGGCTTTTTCTAGGCTTCAGAGCAGGGGAGAG  
CTGGAAGGGGCTAGAAAGCTCCGCTTGTCTGTTTCTCAGGCTCCTGTGAGCCTCAGTCCTG  
AGACCAGAGTCAAGAGGAAGTACACGTCCCAATCACCCGTGTGAGGATTCACTCTCAGGAGC  
TGGGTGGCAGGAGAGGCAATAGCCCCCTGTGGCAATTGCAGGACCAGCTGGAGCAGGGTTGCG  
GTGTCTCCACGGTGCTCTCGCCCTGCCCATGGCCACCCACAGACTCTGATCTCCAGGAACCC  
ATAGCCCCTCTCCACCTACCCCATGTTGATGCCCAGGGTCACTCTTGCTACCCGCTGGGCC  
CCCAAACCCCGCTGCCTCTCTTCCCTTCCCCCATCCCCACCTGGTTTTTGACTAATCCTGC  
TTCCCTCTCTGGGCCTGGCTGCCGGGATCTGGGGTCCCTAAGTCCCTCTCTTTAAAGAACTT  
CTGCGGGTCAGACTCTGAAGCCGAGTTGCTGTGGGCGTGCCCGGAAGCAGAGCGCCACACTC  
GCTGCTTAAGCTCCCCCAGCTCTTTCCAGAAAACATTAAACTCAGAATTGTGTTTTCAA

09444-03101

## **FIGURE 30**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA41234

><subunit 1 of 1, 281 aa, 1 stop

><MW: 31743, pI: 6.83, NX(S/T): 1

MGSRGQGLLLAYCLLLAFASGLVLSRVPHVQGEQQEWEGTEELPSPPDHAERAEEQHEKYRP  
SQDQGLPASRCLRCCDPGTSMPATAVPQINITILKGEKGDRGDRGLQGKYGKTGSAGARGH  
TGPKGQKGSMGAPGERCKSHYAAF SVGRKKPMHSNHYYQTVIFDTEFVNLYDHFNMFTGKFY  
CYVPGLYFFSLNVHTWNQKETYLHIMKNEEEVVILFAQVGDRSIMQSQSLMLELREQDQVWV  
RLYKGERENAIFSEELDTYITFSGYLVKHATEP

### **Signal sequence.**

amino acids 1-25

### **N-glycosylation site.**

amino acids 93-97

### **N-myristoylation sites.**

amino acids 7-13, 21-27, 67-73, 117-123, 129-135

### **Amidation site.**

amino acids 150-154

### **Cell attachment sequence.**

amino acids 104-107

094444-444444

SECRET

CGCGAGCATCCGCTGCGGTCCTCGCCGAGACCCCCGCGGGATTGCGCGGTCCTTCCCGCGG  
GCGCGACAGAGCTGTCTCGCACCTGGATGGCAGCAGGGGCGCCGGGGTCTCTCGACGCCA  
GAGAGAAATCTCATCATCTGTGCGAGCCTTCTTAAAGCAAACCTAAGACCAAGAGGGAGGATTAT  
CCTTGACCTTTGAAGACCAAACTAAACTGAAATTTAAAATGTTCTTCGGGGGAGAAGGGAG  
CTTGACTTACACTTTGGTAATAATTTGCTTCCTGACACTAAGGCTGTCTGCTAGTCAGAATT  
GCCTCAAAAAGAGTCTAGAAGATGTTGTCAATTGACATCCAGTCATCTCTTTCTAAGGGAATC  
AGAGGCAATGAGCCCGTATATACTTCAACTCAAGAAGACTGCATTAATTCTTGCTGTTCAAC  
AAAAAACATATCAGGGGACAAAGCATGTAACCTTGATGATCTTCGACACTCGAAAAACAGCTA  
GACAACCCCACTGCTACCTATTTTTCTGTCCCAACGAGGAAGCCTGTCCATTGAAACCAGCA  
AAAGGACTTATGAGTTACAGGATAATTACAGATTTTCCATCTTTGACCAGAAATTTGCCAAG  
CCAAGAGTTACCCAGGAAGATTCTCTCTTACATGGCCAATTTTCAAGCAGTCACCTCCCC  
TAGCCCATCATCACACAGATTATTCAAAGCCCACCGATATCTCATGGAGAGACACACTTTCT  
CAGAAGTTTGGATCCTCAGATCACCTGGAGAACTATTTAAGATGGATGAAGCAAGTGCCCA  
GCTCCTTGCTTATAAGGAAAAAGGCCATTCTCAGAGTTCACAATTTTCTCTGATCAAGAAA  
TAGCTCATCTGCTGCCTGAAAATGTGAGTGCCTCCCAGCTACGGTGGCAGTTGCTTCTCCA  
CATACCACCTCGGCTACTCCAAGCCCCGCCACCTTCTACCCACCAATGCTTCAGTGACACC  
TTCTGGGACTTCCCAGCCACAGCTGGCCACCACAGCTCCACCTGTAACCACTGTCACTTCTC  
AGCCTCCCACGACCCTCATTTCTACAGTTTTTACACGGGCTGCGGCTACACTCCAAGCAATG  
GCTACAACAGCAGTTCTGACTACCACCTTTCAGGCACCTACGGACTCGAAAGGCAGCTTAGA  
AACCATAACGTTTACAGAAATCTCCAACCTTAACTTTGAACACAGGGAATGTGTATAACCCTA  
CTGCACTTTCTATGTCAAATGTGGAGTCTTCCACTATGAATAAACTGCTTCCTGGGAAGGT  
AGGGAGGCCAGTCCAGGCAGTTCCTCCAGGGCAGTGTTCCAGAAAATCAGTACGGCCTTCC  
ATTTGAAAAATGGCTTCTTATCGGGTCCCTGCTCTTTGGTGTCTGTTCTGGTGATAGGCC  
TCGTCTCTGCGGTAGAAATCCTTTCCGAATCACTCCGCAGGAAACGTTACTCAAGACTGGAT  
TATTTGATCAATGGGATCTATGTGGACATCTAAGGATGGAACCTCGGTGTCTCTTAATTCAAT  
TAGTAACCAGAAGCCCAAATGCAATGAGTTTTCTGCTGACTTGCTAGTCTTAGCAGGAGGTTG  
TATTTTGAAGACAGGAAAATGCCCCCTTCTGCTTTCTTTTTTTTTTTGGAGACAGAGTCTT  
GCTCTGTTGCCCAGGCTGGAGTGCAGTAGCACGATCTCGGCTCTCACCGCAACCTCCGTCTC  
CTGGGTTCAAGCGATTCTCCTGCCTCAGCCTCCTAAGTATCTGGGATTACAGGCATGTGCCA  
CCACACCTGGGTGATTTTTGTATTTTAGTAGAGACGGGGTTTCACCATGTTGGTCAGGCTG  
GTCTCAAACCTCTGACCTAGTGATCCACCCTCCTCGGCCTCCCAAAGTGCTGGGATTACAGG  
CATGAGCCACCACAGCTGGCCCCCTTCTGTTTTATGTTTGGTTTTTTGAGAAGGAATGAAGTG  
GGAACCAAATTAGGTAATTTTGGGTAATCTGTCTCTAAAATATTAGCTAAAAACAAAGCTCT  
ATGTAAAGTAATAAAGTATAATTGCCATATAAATTTCAAATTCAACTGGCTTTTATGCAA  
GAAACAGGTTAGGACATCTAGGTTCCAATTCATTACATTCTTGGTTCAGATAAAATCAAC  
TGTTTTATATCAATTTCTAATGGATTGTCTTTCTTTTTATATGGATTCTTTTAAACTTATT  
CCAGATGTAGTTCTTCCAATTAAATATTTGAATAAATCTTTTGTTACTCAA

## **FIGURE 32**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA45410

><subunit 1 of 1, 431 aa, 1 stop

><MW: 46810, pI: 6.45, NX(S/T): 6

MFFGGEGSLTYTLVIICFLTLRLSASQNCLKKSLEDVVIDIQSSLKSGIRGNEPVYTSTQED  
CINSCCSTKNISGDKACNLMIFDTRKTARQPNCYLFFCPNEEACPLKPAKGLMSYRIITDFP  
SLTRNLPSQELPQEDSLLHGQFSQAVTPLAHHHTDYSKPTDISWRDTLSQKFGSSDHLEKLF  
KMDEASAQLLAYKEKQHSQSSQFSSDQEIAHLLPENVSALPATVAVASPHTTSATPKPATLL  
PTNASVTPSGTSQPQLATTAPPVTTVTSQPPTTLISTVFTRAAATLQAMATTAVLTTTFQAP  
TDSKGSLETIPFTEISNLTNTGNVYNPTALSMSNVESSTMNKTASWEGREASPGSSSQGSV  
PENQYGLPFEEKWLLIGSLLFGVLFLVIGLVLLGRILSESLRRKRYSLDYLINGIYVDI

### **Signal sequence.**

amino acids 1-25

### **Transmembrane domain.**

amino acids 384-405

### **N-glycosylation sites.**

amino acids 72-76, 222-226, 251-255, 327-331, 352-356

### **cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 415-419

### **Tyrosine kinase phosphorylation site.**

amino acids 50-57

### **N-myristoylation sites.**

amino acids 4-10, 48-54, 315-321

094446460



## FIGURE 33

GCGGCACCTGGAAGATGCGCCCATTGGCTGGTGGCCTGCTCAAGGTGGTGTTCGTGGTCTTC  
GCCTCCTTGTGTGCCTGGTATTTCGGGGTACCTGCTCGCAGAGCTCATTCCAGATGCACCCCT  
GTCCAGTGCTGCCTATAGCATCCGCAGCATCGGGGAGAGGCCTGTCCTCAAAGCTCCAGTCC  
CCAAAAGGCAAAAATGTGACCACTGGACTCCCTGCCCATCTGACACCTATGCCTACAGGTTA  
CTCAGCGGAGGTGGCAGAAGCAAGTACGCCAAAATCTGCTTTGAGGATAACCTACTTATGGG  
AGAACAGCTGGGAAATGTTGCCAGAGGAATAAACATTGCCATTGTCAACTATGTAAGTGGGA  
ATGTGACAGCAACACGATGTTTTGATATGTATGAAGGCGATAACTCTGGACCGATGACAAAG  
TTTATTCAGAGTGCTGCTCCAAAATCCCTGCTCTTCATGGTGACCTATGACGACGGAAGCAC  
AAGACTGAATAACGATGCCAAGAATGCCATAGAAGCACTTGGAAGTAAAGAAATCAGGAACA  
TGAAATTCAGGTCTAGCTGGGTATTTATTGCAGCAAAAGGCTTGGAACCTCCCTTCCGAAATT  
CAGAGAGAAAAGATCAACCACTCTGATGCTAAGAACAACAGATATTCTGGCTGGCCTGCAGA  
GATCCAGATAGAAGGCTGCATACCCAAAGAACGAAGCTTGACACTGCAGGGTCCTGAGTAAAT  
GTGTTCTGTATAAAACAAATGCAGCTGGAATCGCTCAAGAATCTTATTTTTCTAAATCCAACA  
GCCCATATTTGATGAGTATTTTGGGTTTGTGTAAACCAATGAACATTTGCTAGTTGTATCA  
AATCTTGGTACGCAGTATTTTTATACCAGTATTTTATGTAGTGAAGATGTCAATTAGCAGGA  
AACTAAAATGAATGGAAATTCTTAAAAAAAAA

0944944.083101

## **FIGURE 34**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA46777

><subunit 1 of 1, 235 aa, 1 stop

><MW: 25982, pI: 9.09, NX(S/T): 2

MRPLAGGLLKVVVFVVFASLCAWYSGYLLAELIPDAPLSSAAYSIRSIGERPVLKAPVPKRQK  
CDHWTPCPSDTYAYRLLSGGGRSKYAKICFEDNLLMGEQLGNVARGINIAIVNYVTGNVTAT  
RCFDMYEGDNSGPMTKFIQSAAPKSLLFMVTYDDGSTRLNNDKNAIEALGSKEIRNMKFRS  
SWVFIAAKGLELPSEIQREKINHSDAKNNRYSGWPAEIQIEGCIPKERS

### **Signal sequence.**

amino acids 1-20

### **N-glycosylation sites.**

amino acids 120-124, 208-212

### **Glycosaminoglycan attachment site.**

amino acids 80-84

### **N-myristoylation sites.**

amino acids 81-87, 108-114, 119-125

004404 083401  
T07E80" H6H660